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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 17, 2003, 22:43:56 ; Search time 1498 Seconds
(without alignments)
11276.297 Million cell updates/sec

Title: US-09-807-933B-13
Perfect score: 1043

Sequence: 1 ggatcctgggacaagatgaa.....cgaaagtaaacgcagatcc 1043

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_estc:*
9: gb_esti:*
10: gb_estc2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estcom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	174.6	16.7	691	10	BE585661
2	133.4	12.8	450	13	BI200729
3	122.2	11.7	444	13	BI190695
4	114.2	10.9	426	13	BI187295
5	83.2	8.0	215	13	BI190568
6	63.4	6.1	606	10	AW057101

7	62.8	6.0	274	13	BI188678
8	62.8	6.0	280	13	BI190362
9	62.8	6.0	289	13	BI189728
10	62.8	6.0	289	13	BI191461
11	62.8	6.0	299	13	BI187393
12	60.8	5.8	500	10	AW565843
13	59.8	5.7	406	10	BE355499
14	59.2	5.7	1490	11	AV103602
15	58.4	5.6	490	14	BQ743825
16	58.4	5.6	605	17	A2640388
17	58.2	5.6	559	13	BM324075
18	58.2	5.6	585	10	BE470936
19	58.2	5.6	607	13	BM323555
20	58.2	5.5	627	12	BG608096
21	57.4	5.5	206	12	BE898613
22	57.2	5.5	582	10	BE583904
23	56.8	5.4	539	13	BM326380
24	56.2	5.4	547	10	AW672247
25	56.2	5.4	610	13	BM324963
26	56.2	5.4	640	10	AV946870
27	56	5.4	487	10	BE367299
28	55.8	5.3	243	10	AW285303
29	55.6	5.3	582	10	AV941765
30	55.6	5.3	584	10	AW671327
31	55.6	5.3	925	17	CNS0091P
32	55.4	5.3	383	12	BF484001
33	55.4	5.3	588	9	AL823173
34	55.4	5.3	648	10	BE517305
35	55.4	5.3	648	13	BM368064
36	55	5.3	401	13	BM348963
37	55	5.3	458	13	BM335613
38	55	5.3	508	13	BM349604
39	55	5.3	539	13	BM336729
40	54.8	5.3	749	14	BQ744212
41	54.6	5.2	577	13	BM075237
42	54.6	5.2	654	14	BQ294885
43	54.6	5.2	668	14	BQ788781
44	54.4	5.2	537	9	AL821349
45	54.4	5.2	619	13	BM442102

ALIGNMENTS

RESULT 1
BE585661
LOCUS
DEFINITION
EST#6PSP6_D02_d2_014 KSU wheat mRNA linear EST 17-AUG-2000
CDNA library Triticum aestivum infected spike
mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Bread wheat.
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Triticum.
REFERENCE
AUTHORS
TITLE
The structure and function of the expressed portion of the wheat
genomes - Kansas State University. Fusarium graminearum infected
spike CDNA library
JOURNAL
COMMENT
Unpublished (2000)
Contact: John Fellers
US Department of Agriculture, Agriculture Research Service, Plant
Science and Entomology Unit
Dept. of Plant Pathology, 4006 Throckmorton Hall, Kansas State
University, Manhattan, KS 66506, USA
Tel: 785-532-2367
Fax: 785-532-6167
Email: jpf@alfalfa.ksu.edu
Sequence have been trimmed to remove vector sequence and low

Wed Jun 18 17:55:22 2003

quality sequence with phred score less than 20

Seq primer: Sp6.

Location/Qualifiers

FEATURES

source

1. .691

/organism="Triticum aestivum"

/cultivar="Sumai3"

/db xref="taxon:4565"

/clone="ESTH6SP6.D02 d2.014"

/clone_lib="KSU wheat Fusarium graminearum infected spike cDNA library"

/tissue type="Spike"

/dev stage="Adult plant"

/lab host="E. coli JM109"

/note="vector: pGEM-T easy; Site 1: SacII; Site 2: SpeI; plants were grown in the greenhouse. Spikes were sprayed with Fusarium graminearum (at what stage). Total RNA, and poly(A) RNA were prepared from infected spikes. cDNA was prepared using the SmartTM PCR cDNA synthesis kit from Clontech. cDNA was cloned into the pGEM-T easy vector from Promega."

BASE COUNT 135 a 196 c 163 g 197 t

ORIGIN

Query Match 16.7%; Score 174.6; DB 10; Length 691;

Best Local Similarity 61.6%; Pred. No. 6.8e-26;

Matches 337; Conservative 0; Mismatches 194; Indels 16; Gaps 3;

QY 395 GTGGCGCTAGCGGCAACCGGCTCACTACCCGCTACTGGAGCTGTGCAAGGCTTCGTCT 454
 Db 160 GIGCTGCTTCTGGAAGTGTCACCTACTCGATAGTGGAGCTGTGCAAGGCTTCGTCT 219
 QY 455 CTTGGCCCGGCAAGGCTTAAGCTCAGCTCGCTGTCTCAAGTCTGCTCAACAAAGAGCGGTCA 514
 Db 220 CTTGGAGTGGCAAGCCAAAGTCAGGCGCCCTGCTTTGACTGTGTGACAAAAGACAAC 279
 QY 515 CGCTCTTAGGACTCCAAAGCCGCTAGTCCGGCTGCAAGCGGCGCAACTCTACATGTGCA 574
 Db 280 CCATCACTAACCTGAAGCGCGTCAACGGTTGTGAGAGTGTGCTTCTGCTTTGTTGA 339
 QY 575 ACACAAACAGGATGGCTGTCAAGCAACCTTGTACGTTTGTGCTTGTGCTTGTGCTTGTGCT 634
 Db 340 CTAACCTACTCCCTTGGGCTGTCAACGACGACCTTGTCTTACGTTTGTCTACTGCTACCAAGC 399
 QY 635 TTAGCGCGGTGCGAGAGCGCTGTGTGCTGTCTTGTCTTGTGCTTGTGCTTGTGCTTGTGCT 694
 Db 400 TTGCTGTGTGCTAGACAGCTGT 459
 QY 695 CCAGCGTTGTGGCAAGAGATGGTCTGAGGTCAACAGCTGCGGCTGACCTTGTGCA 754
 Db 460 GTCCCGTAAAGGGAAGAGATGATGTCCAGTCCCAACACACTGGTGTGTATATTCGGT- 518
 QY 755 GCTCAGCGGTGCGCACTTCGATCTCAGATGCCCGGCGGCGCTGCGCATCTTCAACG 814
 Db 519 -----GATAACCATTTGACCTTATGATGCGCGGCTGTGTGCGGTATATTCGATG 570
 QY 815 GATGCTGTCCAGTGGGCGCTCCCAAACAGCGGTGTGGGCTCGGCTACGCGGCGATCA 874
 Db 571 GATGACCTCTGAGTTCGGCAAGCCCTCG-----GTGGTGTCTAGTACGCGGCGATCT 624
 QY 875 GCTCGGCGAGCACTGCTCGTCCCTCCAGCGGCTTCCAGGCGGCTGCAAGTGGCGCT 934
 Db 625 CTTTCCGAGGCA-TGTGACAGTTTCCCGGAGTGTCTCAGGATGGTTGCACTGCGGAT 683
 QY 935 TCAACTG 941
 Db 684 TTGACTG 690

RESULT 2

BI200729

LOCUS

DEFINITION

BI200729 450 bp mRNA linear EST 10-JUL-2001
 olf05fs.r1 Fusarium sporotrichioides Tri 10 overexpressed cDNA
 library Fusarium sporotrichioides cDNA clone olf05fs 5', mRNA

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

sequence.

BI200729 GI:14666701

EST.

Fusarium sporotrichioides.

Fusarium sporotrichioides.

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Hypocreales; mitosporic Hypocreales; Fusarium.

1 (bases 1 to 450)

Ren,Q., Tag,A., Peplow,A., Lai,H., Kupfer,C., Peterson,A., Beremand

,M. and Roe,B.

Analysis of a Fusarium sporotrichioides EST database

Unpublished (2001)

Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu

Department of Chemistry and Biochemistry

Advanced Center for Genome Technology, University of Oklahoma

620 Parrington Oval, Norman, OK 73019, USA

Tel: 405 325 4912

Fax: 405 325 7762

Email: broe@ou.edu

Contact Dr. Marian Beremand regarding clone availability Included

is the best homolog from a blastx search of Genbank nr 04-09-01

633 5e-66 g|1170140|sp|P45699 PUTATIVE ENDOGLUCANASE TYPE

KPECURSOR [EN

Seq primer: T3

High quality sequence stop: 440.

Location/Qualifiers

FEATURES

source

1. .450

/organism="Fusarium sporotrichioides"

/strain="Tri 10"

/db xref="taxon:5514"

/clone="olf05fs"

/clone_lib="Fusarium sporotrichioides Tri 10 overexpressed cDNA library"

/note="vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript

; 3' end of cDNA cloned into XhoI site of pBluescript"

BASE COUNT 90 a 125 c 102 g 133 t

ORIGIN

Query Match 12.8%; Score 133.4; DB 13; Length 450;

Best Local Similarity 63.0%; Pred. No. 1.7e-17;

Matches 206; Conservative 0; Mismatches 121; Indels 0; Gaps 0;

QY 395 GTGGCGCTAGCGGCAACCGGCTCACTACCCGCTACTGGAGCTGTGCAAGGCTTCGTCT 454
 Db 124 GTGCTCTTCTGGAAGTGCCACTCTACTCGATAGTGGAGCTGTGCAAGGCTTCGTCT 183
 QY 455 CGTGGCCCGGCAAGGCTTAAGCTCAGCTCGCTGTCAAGTCTCTGCAACAAAGAGCGGTCA 514
 Db 184 CTTGGAGCGGCAAGGCTAAAGTCAGGCGCCCTGCTGTGCTGTGCAACAAAGATAACC 243
 QY 515 CGCTCTTAGCGACTCCAAAGCGGCTGCGGCTGCAAGCGGCGCAACTCTTACATGTGCA 574
 Db 244 CTATCACTAACCTGAAGCTGTCAACGGTTGTGAGGGTGTGCTTCTGTATGCTTGA 303
 QY 575 ACACAAACAGCATGGGCTGTCAAGCAACTTGTCTTACGTTTGTGCTGCGCTGCGCA 634
 Db 304 CCAACTACTCCCGTGGGCTGTCAAGCAACTTGTCTTACGTTTGTGCTGCTTACCAAGC 363
 QY 635 TTACGCGGCTGGCGAGAGCGGCTGGTGTGCTTCTGCTTGTGAGCTCACCTTCACTCCA 694
 Db 364 TTGCTGGTGTAGTAGGCGGCTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 423
 QY 695 CCAGCGTGTGGCAAGATGTCG 721
 Db 424 GTCCCGTGAGGCGCAAGAGATGATTG 450

RESULT 3

BI190695

LOCUS

DEFINITION

BI190695 444 bp mRNA linear EST 10-JUL-2001
 i3g10fs.r1 Fusarium sporotrichioides Tri 10 overexpressed cDNA

library Fusarium sporotrichioides cDNA clone i3g10fs 5', mRNA
sequence.
B1190695
VERSION B1190695.1 GI:14664374
KEYWORDS
SOURCE
ORGANISM
Fusarium sporotrichioides.
Fusarium sporotrichioides
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; mitosporic Hypocreales; Fusarium.
1 (bases 1 to 444)
REFERENCE
AUTHORS Ren,Q., Tag,A., Peplow,A., Lai,H., Kupfer,C., Peterson,A., Beremand
,M. and Roe,B.
TITLE Analysis of a Fusarium sporotrichioides EST database
JOURNAL Unpublished (2001)
COMMENT Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
Contact Dr. Marian Beremand regarding clone availability Included
is the best homolog from a blastx search of Genbank nr 04-09-01
576 3e-59 gi|1170140|sp|P45699 PUTATIVE ENDOGLUCANASE TYPE
KPRECURSOR (EN
Seq primer: T3.
Location/Qualifiers
1..444
/organism="Fusarium sporotrichioides"
/strain="Tri 10"
/db_xref="taxon:5514"
/clone="i3g10fs"
/clone_lib="Fusarium sporotrichioides Tri 10 overexpressed
cDNA library"
/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript
; 3' end of cDNA cloned into XhoI site of pBluescript"
BASE COUNT 85 a 127 c 92 g 140 t
ORIGIN

Query Match 11.7%; Score 122.2; DB 13; Length 444;
Best Local Similarity 63.4%; Pred. No. 3.3e-15;
Matches 187; Conservative 0; Mismatches 108; Indels 0; Gaps 0;
QY 395 GTGGCGCTAGCGCAAGCGCTCACTACCGCTACTGGGACTGCTGCAAGGCTTCTGTCT 454
DB 150 GTGCTCTTCTGAACTGGCCACTCTACTCGATCTGGGACTGCTGCAAGGCTTCTGTCT 209
QY 455 CGTGGCCCGCAAGGCTAAGCTCAGCTCGCCTGTCAAGTCTCTGCAACAAGGACGGGTCA 514
DB 210 CTTGGAGCGCAAGGCTAAGTCAAGTCAGCGCCCTGCTGCTGACTTGTGACACAAGATAACC 269
QY 515 CGCTCTTAGCGACTCAAGCGCAGTCCGGCTGCAACGGCGGCAACTCTCATGTGCA 574
DB 270 CTATCACTAACCTGAACCGTGTCAACGGTTGTGAGGGTGTGTCTGCTTATGCTTGA 329
QY 575 ACACAAACAGCCATCGGCTGTCAACGACAACTTGTACGGTTTTCGCTGCGGTGCCA 634
DB 330 CCAACTACTCCCGTGGGCTGTCAACGACAACTTGTACGGTTTTCGCTGCTACCAAGC 389
QY 635 TTAGCGCGGTGGCGAGAGCGGCTGTGCTGCTCTCTGCTTTCGAGCTCACCTTTCAC 689
DB 390 TTGCTGGTGTAGTGAGGCCAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 444

RESULT 4
B1187295
LOCUS
DEFINITION B1187295 426 bp mRNA linear EST 10-JUL-2001
alhlifs.r1 Fusarium sporotrichioides Tri 10 overexpressed cDNA
library Fusarium sporotrichioides cDNA clone alhlifs 5', mRNA
sequence.
ACCESSION B1187295
VERSION B1187295.1 GI:14660974

KEYWORDS
SOURCE
ORGANISM
Fusarium sporotrichioides.
Fusarium sporotrichioides
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; mitosporic Hypocreales; Fusarium.
1 (bases 1 to 426)
REFERENCE
AUTHORS Ren,Q., Tag,A., Peplow,A., Lai,H., Kupfer,C., Peterson,A., Beremand
,M. and Roe,B.
TITLE Analysis of a Fusarium sporotrichioides EST database
JOURNAL Unpublished (2001)
COMMENT Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
Contact Dr. Marian Beremand regarding clone availability Included
is the best homolog from a blastx search of Genbank nr 04-09-01
565 5e-58 gi|1170140|sp|P45699 PUTATIVE ENDOGLUCANASE TYPE
KPRECURSOR (EN
Seq primer: T3
High quality sequence stop: 338.
Location/Qualifiers
1..426
/organism="Fusarium sporotrichioides"
/strain="Tri 10"
/db_xref="taxon:5514"
/clone="alhlifs"
/clone_lib="Fusarium sporotrichioides Tri 10 overexpressed
cDNA library"
/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript
; 3' end of cDNA cloned into XhoI site of pBluescript"
BASE COUNT 82 a 119 c 91 g 134 t
ORIGIN

Query Match 10.9%; Score 114.2; DB 13; Length 426;
Best Local Similarity 62.4%; Pred. No. 1.4e-13;
Matches 179; Conservative 0; Mismatches 108; Indels 0; Gaps 0;
QY 395 GTGGCGCTAGCGCAAGCGGCTCACTACCGCTACTGGGACTGCTGCAAGGCTTCTGTCT 454
DB 140 GTGCTGCTTCTGAAAGTGCCACTCTACTCGATCTGGGACTGCTGCAAGGCTTCTGTCT 199
QY 455 CGTGGCCCGCAAGGCTAAGCTAAGTCAAGTCTGCTGCTGCAACAAGGACGGGTCA 514
DB 200 CTTGGAGCGCAAGGCTAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 259
QY 515 CGCTCTTAGCGACTTCAACGCGCCAGTCCGGCTGCAACGGCGGCAACTCTCATGTGCA 574
DB 260 CTATCACTAACCTGAACCGTGTCAACGGTTGTGAGGGTGTGTCTGCTTATGCTTGA 319
QY 575 ACACAAACAGCCATCGGCTGTCAACGACAACTTGTACGGTTTTCGCTGCGGTGCCA 634
DB 320 CCAACTACTCCCGTGGGCTGTCAACGACAACTTGTACGGTTTTCGCTGCTACCAAGC 379
QY 635 TTAGCGCGGTGGCGAGAGCGGCTGTGCTGCTCTCTGCTTTCGAGCTC 681
DB 380 TTGCTGGTGTAGTGAGGCCAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 426

RESULT 5
B1190568
LOCUS
DEFINITION B1190568 215 bp mRNA linear EST 10-JUL-2001
i2ellifs.r1 Fusarium sporotrichioides Tri 10 overexpressed cDNA
library Fusarium sporotrichioides cDNA clone i2ellifs 5', mRNA
sequence.
ACCESSION B1190568
VERSION B1190568.1 GI:14664247
KEYWORDS
SOURCE Fusarium sporotrichioides.

ORGANISM Fusarium sporotrichioides
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; mitosporic Hypocreales; Fusarium.

REFERENCE 1 (bases 1 to 215)
AUTHORS Ren,Q., Tag,A., Peplow,A., Lai,H., Kupfer,C., Peterson,A., Beremand,
M., and Roe,B.

TITLE Analysis of a Fusarium sporotrichioides EST database
JOURNAL Unpublished (2001)
COMMENT Other_ESTs: i2ellfs.fl
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
Contact Dr. Marian Beremand regarding clone availability Included
is the best homolog from a blastx search of Genbank nr 04-09-01
363 76-35 gi|1170140|sp|p45699 PUTATIVE ENDOGLUCANASE TYPE
KPRECURSOR [EN
Seq primer: T3
High quality sequence stop: 156.

FEATURES
source Location/Qualifiers
1..225
/organism="Fusarium sporotrichioides"
/strain="Tri 10"
/db_xref="taxon:5514"
/clone="i2ellfs"
/clone_lib="Fusarium sporotrichioides Tri 10 overexpressed
cDNA library"
/note="vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript"
3' end of cDNA cloned into XhoI site of pBluescript"
BASE COUNT 44 a 61 c 53 g 56 t 1 others
ORIGIN
Query Match 8.0%; Score 83.2; DB 13; Length 215;
Best Local Similarity 63.5%; Pred. No. 2.6e-07;
Matches 127; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 427 TACTGGGACTGCTGCAGGCTTGCTGCTGTGCCCCGCAAGCTTAACGTCAAGCTCGCT 486
Db 1 TACTGGGACTGCTGCAGGCTTCTTGCTCTTGGAGCGGCAAGCTTAAGTCAGCGCCCT 60

QY 487 GTCAAGTCTGTCAACAGGCGGCTCACCGCTCTTAGCGACTCCAAAGCCCGAGTCGCGC 546
Db 61 GCTCTGACTGTGACACAAAGATTAACCTATCACTAACGTGAAGCTGTCAACGGTTGT 120

QY 547 TGCACAGCGCGGCAACTCTTACATGTGACACACACACAGGCATGGCTGTCAACGACAC 606
Db 121 GAGGGTGGTGGTTCTTGCTTATGCTTGCACCAACTACTCCCGGTGGGCTGTCAACGAC 180

QY 607 CTTCGCTTACGGTTTCGCTGC 626
Db 181 CTTCGCTTACGGTTTCGCTGC 200

RESULT 6
AW057101 606 bp mRNA linear EST 29-SEP-1999
LOCUS 60008G01.y1 660 - Mixed stages of anther and pollen Zea mays cDNA
DEFINITION mRNA sequence.
ACCESSION AW057101
VERSION AW057101.1 GI:5932740
KEYWORDS EST.
SOURCE Zea mays.
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 606)
WALBOT,V.
TITLE Mailbox ESTs from various cDNA libraries sequenced at Stanford

ORGANISM Fusarium sporotrichioides
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; mitosporic Hypocreales; Fusarium.

REFERENCE 1 (bases 1 to 274)

AUTHORS Ren,Q., Tag,A., Peplow,A., Lai,H., Kupfer,C., Peterson,A., Beremand
,M. and Roe,B.

TITLE Analysis of a Fusarium sporotrichioides EST database

JOURNAL Unpublished (2001)

COMMENT Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu

Contact Dr. Marian Beremand regarding clone availability Included
is the best homolog from a blastx search of Genbank nr 04-09-01
303 1e-27 gi|1170140|sp|p45699 PUTATIVE ENDOGLUCANASE TYPE

KPRECURSUS (EN
Seq primer: T3
High quality sequence stop: 102.

FEATURES
source
1..274
Location/Qualifiers
/organism="Fusarium sporotrichioides"
/strain="Tri 10"
/db_xref="taxon:5514"
/clone="d2c10fs"
/clone_lib="Fusarium sporotrichioides Tri 10 overexpressed
cDNA library"
/note="Vector: pBlueScript SK-; Site_1: EcoRI; Site_2:
XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript
XhoI; 3' end of cDNA cloned into XhoI site of pBluescript"

BASE COUNT 62 a 80 c 49 g 83 t

ORIGIN
Query Match 6.0%; Score 62.8; DB 13; Length 274;
Best Local Similarity 71.9%; Pred. No. 0.0044;
Matches 82; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 395 GTGGCGCTAGCGCAACGGGTCACTACCGCTACTGGGACTGCTCAAGGCTTCGTCT 454
Db 127 GTGCTCTTCTGGAAGTGGCACTTACTCGATCTGGGACTGCTCAAGGCTTCGTCT 186

QY 455 CGTGGCCGCGCAAGGCTAAGTCAGCTCGCTCAAGTCTCAAGTCTCAACAAAGGACG 508
Db 187 CTGGAGCGCGCAAGGCTAAGTCAGCGCCCTCTGACTTGTGACACAAAG 240

RESULT 8
BI190362
LOCUS 280 bp mRNA linear EST 10-JUL-2001
DEFINITION h4h07fs.r1 Fusarium sporotrichioides Tri 10 overexpressed cDNA
library Fusarium sporotrichioides CDNA clone h4h07fs 5', mRNA
sequence.

ACCESSION BI190362
VERSION BI190362.1 GI:14664041
KEYWORDS EST.
SOURCE Fusarium sporotrichioides.
ORGANISM Fusarium sporotrichioides
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; mitosporic Hypocreales; Fusarium.

REFERENCE 1 (bases 1 to 280)

AUTHORS Ren,Q., Tag,A., Peplow,A., Lai,H., Kupfer,C., Peterson,A., Beremand
,M. and Roe,B.

TITLE Analysis of a Fusarium sporotrichioides EST database

JOURNAL Unpublished (2001)

COMMENT Other ESTs: h4h07fs.f1
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762

Email: broe@ou.edu
Contact Dr. Marian Beremand regarding clone availability Included
is the best homolog from a blastx search of Genbank nr 04-09-01
303 1e-27 gi|1170140|sp|p45699 PUTATIVE ENDOGLUCANASE TYPE

KPRECURSUS (EN
Seq primer: T3
High quality sequence stop: 261.

FEATURES
source
1..280
Location/Qualifiers
/organism="Fusarium sporotrichioides"
/strain="Tri 10"
/db_xref="taxon:5514"
/clone="h4h07fs"
/clone_lib="Fusarium sporotrichioides Tri 10 overexpressed
cDNA library"
/note="Vector: pBlueScript SK-; Site_1: EcoRI; Site_2:
XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript
XhoI; 3' end of cDNA cloned into XhoI site of pBluescript"

BASE COUNT 60 a 79 c 53 g 88 t

ORIGIN
Query Match 6.0%; Score 62.8; DB 13; Length 280;
Best Local Similarity 71.9%; Pred. No. 0.0045;
Matches 82; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 395 GTGGCGCTAGCGCAACGGGTCACTACCGCTACTGGGACTGCTCAAGGCTTCGTCT 454
Db 133 GTGCTCTTCTGGAAGTGGCACTTACTCGATCTGGGACTGCTCAAGGCTTCGTCT 192

QY 455 CGTGGCCGCGCAAGGCTAAGTCAGCTCGCTCAAGTCTCAAGTCTCAACAAAGGACG 508
Db 193 CTGGAGCGCGCAAGGCTAAGTCAGCGCCCTCTGACTTGTGACACAAAG 246

RESULT 9
BI189728
LOCUS 289 bp mRNA linear EST 10-JUL-2001
DEFINITION g1c06fs.r1 Fusarium sporotrichioides Tri 10 overexpressed cDNA
library Fusarium sporotrichioides CDNA clone g1c06fs 5', mRNA
sequence.

ACCESSION BI189728
VERSION BI189728.1 GI:14663407
KEYWORDS EST.
SOURCE Fusarium sporotrichioides.
ORGANISM Fusarium sporotrichioides
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; mitosporic Hypocreales; Fusarium.

REFERENCE 1 (bases 1 to 289)

AUTHORS Ren,Q., Tag,A., Peplow,A., Lai,H., Kupfer,C., Peterson,A., Beremand
,M. and Roe,B.

TITLE Analysis of a Fusarium sporotrichioides EST database

JOURNAL Unpublished (2001)

COMMENT Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu

Contact Dr. Marian Beremand regarding clone availability Included
is the best homolog from a blastx search of Genbank nr 04-09-01
303 1e-27 gi|1170140|sp|p45699 PUTATIVE ENDOGLUCANASE TYPE

KPRECURSUS (EN
Seq primer: T3
High quality sequence stop: 272.

FEATURES
source
1..289
Location/Qualifiers
/organism="Fusarium sporotrichioides"
/strain="Tri 10"
/db_xref="taxon:5514"
/clone="g1c06fs"
/clone_lib="Fusarium sporotrichioides Tri 10 overexpressed
cDNA library"

BASE COUNT	ORIGIN	Query Match	Best Local Similarity	Matches	Score	DB 13;	Length	289;	
64 a	84 c	49 g	92 t	0; Mismatches	32;	Indels	0;	Gaps	0;
395	GTGGCGCTAGCGCAACGGCGTCACTACCGCGTACTGGGACTGCTGCAAGGCTTCGTGCT	454							
142	GTGCTGTTCTTGGAGTGGCCACTCTACTCGATACGATACGCGACTGCTGCAAGCTTCCTGCT	201							
455	CGTGGCCCGGACGCTTAAGCTGAGCTCGCGTCTCAAGTCTCTGCACACAGGACG	508							
202	CTTGGAGCGGACGCTTAAGTACGAGCCCTGCTCTGACTGTGTGACACAAAG	255							
RESULT 10									
BI191461	289 bp mRNA	linear	EST 10-JUL-2001						
LOCUS	k3g10fs.r1	Fusarium sporotrichioides Tri 10 overexpressed cDNA							
DEFINITION	library Fusarium sporotrichioides cDNA clone k3g10fs 5', mRNA								
ACCESSION	sequence.								
VERSION	BI191461								
KEYWORDS	EST.								
SOURCE	Fusarium sporotrichioides.								
ORGANISM	Fusarium sporotrichioides.								
REFERENCE	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;								
AUTHORS	Hypocreales; mitosporic Hypocreales; Fusarium.								
	1 (bases 1 to 289)								
	Ren, Q., Tag, A., Peplow, A., Lai, H., Kupfer, C., Peterson, A., Beremand								
	, M. and Roe, B.								
TITLE	Analysis of a Fusarium sporotrichioides EST database								
JOURNAL	Unpublished (2001)								
COMMENT	Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu								
	Department of Chemistry and Biochemistry								
	Advanced Center for Genome Technology, University of Oklahoma								
	620 Parrington Oval, Norman, OK 73019, USA								
	Tel: 405 325 4912								
	Fax: 405 325 7762								
	Email: broe@ou.edu								
	Contact Dr. Marian Beremand regarding clone availability Included								
	is the best homolog from a blastx search of Genbank nr 04-09-01								
	321 Es-30 [g11170140]sp P45699 PUTATIVE ENDOGLUCANASE TYPE								
	XPRECURSOR (EN								
	Seq primer: T3								
	High quality sequence stop: 265.								
FEATURES									
source	Location/Qualifiers								
1..289	/organism="Fusarium sporotrichioides"								
	/strain="Tri 10"								
	/db_xref="taxon:5514"								
	/clone="k3g10fs"								
	/cna_lib="Fusarium sporotrichioides Tri 10 overexpressed								
	cDNA library"								
	/note="Vector: pBlueScript SK-; Site 1: EcoRI; Site 2:								
	/note: 5' end of cDNA cloned into EcoRI site of pBlueScript								
	; 3' end of cDNA cloned into XhoI site of pBlueScript"								
62 a	81 c	56 g	90 t						
BASE COUNT									
ORIGIN									
Query Match	6.0%;	Score 62.8;	DB 13;	Length 289;					
Best Local Similarity	71.9%;	Pred. No. 0.0045;							
Matches	82; Conservative	0; Mismatches	32;	Indels	0;	Gaps	0;		
395	GTGGCGCTAGCGCAACGGCGTCACTACCGCGTACTGGGACTGCTGCAAGGCTTCGTGCT	454							
133	GTGCTGTTCTTGGAGTGGCCACTCTACTCGATACGATACGCGACTGCTGCAAGCTTCCTGCT	192							
455	CGTGGCCCGGACGCTTAAGCTGAGCTCGCGTCTCAAGTCTCTGCACACAGGACG	508							

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Sorghum.

REFERENCE
1 (bases 1 to 500)
AUTHORS Cordonnier-Pratt M.-M., Gingle, A., Marsala C. and Pratt, L.H.
TITLE An EST database from Sorghum: light-grown seedlings
JOURNAL Unpublished (2000)

Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210

Email: mmpratt@uga.edu
Sequences have been trimmed below Phred quality 16. The threshold for highest quality sequence is 20.

High quality sequence start: 500
High quality sequence stop: 500

FEATURES	Location/Qualifiers
source	1...500
POLYA=Yes.	
sequence	
seq. no.	
seq. type	
seq. length	
seq. start	
seq. stop	
seq. step	

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/db_xref="taxon:4558"
/collection="Light Green 1 (LC1)"

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/clone_lib="Light Grown 1 (LG1)"
/note="Organ: 10- to 14-day-old light-grown (greenhouse)
seedlings. Vector: lambda Zap. Site 1: Vho1 Site 2: EcoRI"
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BASE COUNT	122 a	143 c	119 g	115 t	1 others
ORIGIN					

Query Match 5.8%; Score 60.4; DB 10; Length 500;
Best Local Similarity 56.3%; Pred. No. 0.017;
Matches 112; Conservative 0; Mismatches 87; Indels 0; Gaps 0

COMMENT

Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1960
Fax: 706 583 0210
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions below Fired quality 16. The threshold for highest quality sequences is 20.

Seq primer: POLYTWix
High quality sequence start: 3
High quality sequence stop: 398
POLYA=N3.

FEATURES

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/organism="Sorghum bicolor"
/db_xref="taxon:4558"
/clone_lib="Dark Grown 1 (DGL)"
/note="Organ: 5-day-old dark-grown seedlings; Vector:
lambda Zap; Site 1: XhoI; Site 2: EcoRI. The library was
made from poly-A RNA in the cloning vector lambda ZAP II.
Clones to be sequenced were prepared by mass excision."
97 a 122 c 105 g 82 t
BASE COUNT

```

ORIGIN	Query Match	5.7%	Score 59.8	DB 10	Length 406
--------	-------------	------	------------	-------	------------

Best Local Similarity	56.3%;	Pred. No. 0.021;	Score 3310; SE 10;	Mean 100;
Matches 112: Conservative	0;	Mismatches 87;	Indels 0;	Gaps 0

OV 24 CATCACATATCGCCTCCTCCGCC

24
47
Db
Qy
Db

96
84
156

CACCCCACCCCTGCAGGAGCAGCACCTGGTTCTTCCACTCCACACACCCCC
CGCTGAGTCTCCAAAGTCTACGGACAGTCGGCGGGAAGAACTGGAAACGCGCCCCCACTG
TGCCGCGACGCTCGACCAGTGGGACAGTCGGCTGGTCAGAACTACACGCGCCCCCAACGAC

155
143
215

Qy	144	CTGCGAGCGGCTCGACCTCGAAGTCTCAATGACTTACTACAGCAGTGCCTGCCGAG	203
Db	216	CTGCAAGTCTCCCTTCACCTCGAAGAGATCAACGACTTTCTACCCAGTGCCAGTAAAG	275
Qy	204	CGGCTCCTCGGGAACAAG	222

Dbb 276 GGGCTGCCAGCTATCTAG 294

/db_xref="MaizeDB:635311"
 /db_xref="taxon:4577"
 /clone="PC093211"
 /clone_lib="Maize Mapping Project/DuPont Cornsensus Library"
 /note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"

BASE COUNT 301 a 528 c 405 g 256 t
 ORIGIN

Query Match 5.7%; Score 59.2; DB 11; Length 1490;
 Best Local Similarity 45.0%; Pred. No. 0.044;
 Matches 223; Conservative 0; Mismatches 273; Indels 0; Gaps 0;
 QY 498 CAACAAGACGGCGTCAACGCTCTTAGGAGTCCCAAGCCGAGTCCGGCTGCAACGGGG 557
 DB 369 CAAGTACGACTCCACGCTGGCATCTTCAGCGCGAGTCAAGCCGTCGGGCAACAGC 428
 QY 558 CAATCTTACATGTGCAAGACCAACGACCATGGCTGTCAAGACAACTTGTTCAGG 617
 DB 429 CATCTTCCTGACGGCAAGTATCAAGTGTGTTCGACGCAACCCAGCAACTGCC 488
 QY 618 TTTCCTCCGCTCCATAGCGCGGTGGCGAGAGCGGTGTGTCTCTCTCTTCA 677
 DB 489 GTGGGGGAGTCTGGCATGACCTGTATGAGGGGACCGGGCTTCTGTGACCGGA 548
 QY 678 GCTACCTTACCTCCACAGGCTTGTGGCAAGAGATGTCGTCCAGTCAACAC 737
 DB 549 GGGCGGGGAAGACATCCAGCGGGGGCCCAAGAAGTGTCTCATCAGCGGCCGGCAA 608
 QY 738 TGGCGGTGACCTTGGAGCTTCAGCGGTGCCACTTGCATCTCCAGTCCAGTCCGCGGGGG 797
 DB 609 GGGCGACATCCCACTTACGCTGTGGGTCAATGCCGACCAAGTACCAACCCGAGACCC 668
 QY 798 CQTGGGATCTTCAAGGATGTCGTCGCCAGTGGGGGCTCCCAAGCAGCGGTGGGGTCC 857
 DB 669 CATCATAGCAAGCGCTCTGCAACCAACCACTGCTCGCGCCATTGTCAGGTCCTCGA 728
 QY 858 GCGCTACGGGGATGATCCGACGAGTGTGTGCTCCCGAGCGGCTCCAGCGCTCCAGGC 917
 DB 729 CCAGAAGTTCGGCATCATCAAGGCGACCATGACACCACTTCTTACCGCGGACCA 788
 QY 918 CGGCTGCAAGTGGCGCTTCACTGTGTTCAAGAACCGCGACACCGTTCATGACCTCAA 977
 DB 789 GAGGCTGTGGAACGCGAGCACCGGACCTGCGCGCGCGCGCGCGCGCTCAACAT 848
 QY 978 GGAGGTACCTGCGCC 993
 DB 849 CGTGGCCACATCCACC 864

RESULT 15
 B0743825
 LOCUS 490 bp mRNA linear EST 17-JUL-2002
 DEFINITION WHE4108_E11_J22ZS wheat salt-stressed root cDNA library Triticum aestivum cDNA clone WHE4108_E11_J22, mRNA sequence.
 ACCESSION B0743825
 VERSION B0743825.1 GI:21890612
 KEYWORDS EST.
 SOURCE bread wheat.
 ORGANISM Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Triticum.
 1 (bases 1 to 490)
 REFERENCE Anderson, O.D., Akhunov, E., Chao, S., Crossman, C., Deal, K., Dvorak, J., Lazo, G.R., Pham, J., Rausch, C.J., Wilson, C. and Woo, J.
 The structure and function of the expressed portion of the wheat genomes - Salt-stressed root cDNA library

JOURNAL COMMENT

Unpublished (2002)
 Contact: Olin Anderson
 US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center
 800 Buchanan Street, Albany, CA 94710, USA
 Tel: 5105595773
 Fax: 5105595818
 Email: oanderson@ow.usda.gov
 Sequences have been trimmed to remove vector sequence and low quality sequence with phred score less than 20
 Seq primer: SK primer

FEATURES source

1..490
 /organism="Triticum aestivum"
 /cultivar="Chinese Spring"
 /db_xref="taxon:4565"
 /clone="WHE4108_E11_J22"
 /clone_lib="Wheat salt-stressed root cDNA library"
 /tissue_type="Roots"
 /dev_stage="Full tillering"
 /lab_host="E. coli SOLR"
 /note="Vector: Lambda Uni-ZAP XR, excised phagemid pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; Hydroponic plants grown to full tillering stage were treated with 150 mM NaCl for either 12 hours or 7 days. Root tissues of the plants subjected to both types of treatment were collected separately at University of California, Davis (E. Akhunov and K. Deal in J. Dvorak's lab). Total RNA was prepared and equal amount of RNA was then pooled. PolyA RNA was purified from the pooled RNA, a cDNA library was made, and the cDNA clones were in vivo excised to give pBluescript SK(-) phagemids in J. Dvorak's lab (E. Akhunov, J. Dvorak) at the University of California, Davis. Colony plating, plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."

BASE COUNT 85 a 196 c 167 g 42 t
 ORIGIN

Query Match 5.6%; Score 58.4; DB 14; Length 490;
 Best Local Similarity 47.3%; Pred. No. 0.044;
 Matches 176; Conservative 0; Mismatches 196; Indels 0; Gaps 0;
 QY 307 CCGCCAGAGAGACGACGCTGCGCAAGGCTTCGACTCCGTCCTCAACTCGAGCAGCTCG 366
 DB 66 CAGAGCTGGCGCCAGAGAGCTCGACAGAGCGGCGCGCCGCTGCGGGCGGCGC 125
 QY 367 TCTTGGGAAAGTACAGCGTGTACGGTGGCGTACGGGAAACGGGCTACTACCGCG 426
 DB 126 GCGACCGGCTGCGCGCTCGCGCTCGCGCGCGGCAACGCGGGGCGCTCGGGCGCAC 185
 QY 427 TACTGGGACTGTGCAAGGCTTCGTCTGTGCGCCCGGAAGGCTAACGTGAGCTCGCCT 486
 DB 186 TACCGCGCGTCAGAGAGCGCGCTGGGGCGGTATACGGCGGAGATCCGCGACCGCGCC 245
 QY 487 GTCAAGTCTGCAAGAGGAGCGGCTCACGCTCTTAGCGACTCCAAACGCGCAAGTCCGGC 546
 DB 246 AAGAGAGCGGGTGTGGCTCGGACAGTACGACGCGGAGGCGCGCGGCTAC 305
 QY 547 TGTCAAGCGGCAACTCTACATGTCAACGACCAACGACCATGGCTGTCAACGACAC 606
 DB 306 GAGCGCGCGCGGAGTACCGGGCAACAGGCGCAAGCACTTCCCTTTCGCTCC 365
 QY 607 CTTGCTTACGGTTTCTGTCGGTGTGCTTACGCGGTGTGGGAGAGCGGCTGTGTGTC 666
 DB 366 GCTCTCGCGCGCGCGCGCGCGCGCGCGCTTACCGCGGAGCGCGGAGCGCAACAGC 425
 QY 667 TCTGCTTTCGAG 678
 DB 426 AGCAGCGTTCGAG 437.

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Wed Jun 18 17:55:22 2003

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